Patent Docket P1084R1-2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

jc518 U.S. PTO 09/107979 06/30/98

In re Application of Paul J. Godowski et al. Serial No.: To be assigned Filed: 30 June 1998 (Filed Herewith) For: ErbB4 Receptor-Specific Neuregulin Related Ligands and Uses Therefor	Group Art Unit: Unassigned Examiner: Unassigned CERTIFICATION UNDER 37 CFR 1.10 EM 168 883 749 US: Express Mail Number June 30 1998: Date of Deposit I hereby certify that this correspondence, consisting of CERTIFICATE RE: SEQUENCE LISTING RESPONSE UNDER 37 CFR § 1.821(f) and (g), paper copy and a computer-readable diskette, is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner of Patents, Washington, D.C. 20231. Pamela Gavette Pamela Gavette

CERTIFICATE RE: SEQUENCE LISTING

RESPONSE UNDER 37 CFR § 1.821(f) and (g)

BOX PATENT APPLICATION
Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the content of the paper and computer readable copies are the same. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

Date: June 30, 1998

By: _____
Deirdre L. Conley, Ph.D.
Reg. No. 36,487

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This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Unassigned
(B) FILING DATE: 30-Jun-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Conley, Deirdre L.
(B) REGISTRATION NUMBER: 36,487
(C) REFERENCE/DOCKET NUMBER: P1084R1-2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-2066
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2538 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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(ix) FEATURE:
      (A) NAME/KEY: mouse NRG3 nucleic acid
      (B) LOCATION: 1-2538
      (C) IDENTIFICATION METHOD:
      (D) OTHER INFORMATION:

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:


CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50

TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100

CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150

GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200

GCCCGCGCCC GCGCCCGCGC CCGGCCCGCG CGGCCCCATG CCTCTGGCGC 250

GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300

GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350

CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400

CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCCGGGA GTTACGCTGT 450

AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500

TCTGTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550

GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCCACGGA CCTGGTGGAC 600

TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650

CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700

CCACCCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750

AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800

CCGGGTTCCC ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850

CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900

ACGCCCGGCT CCCGACCCCC GATGCCAGGA GCCCCCAGTA CGCAGGCGAT 950

GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000

CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050

TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100
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102    ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200
103
104    GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
105
106    CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
107
108    ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
109
110    AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTCAT GTATCATCTT 1400
111
112    TGGAATTGTC ATCGTGGGCA TGTTCTGTGC AGCATTCTAC TTCAAAAGCA 1450
113
114    AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
115
116    AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
117
118    GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
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120    CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650
121
122    CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
123
124    CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750
125
126    CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
127
128    CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
129
130    GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
131
132    TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
133
134    CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
135
136    TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
137
138    CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
139
140    CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACTC 2150
141
142    CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
143
144    TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
145
146    ATCCGGATTC TGACTGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
147
148    CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
149
150    GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400
151
152    ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
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GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:
(A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
(B) LOCATION: 1-713
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
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Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
            20                  25                  30

Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
        35                  40                  45

Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
    50                  55                  60

Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
65                  70                  75

Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
            80                  85                  90

Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
        95                  100                 105

Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
    110                 115                 120

Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
125                 130                 135

Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
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Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
        155                 160                 165
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206  Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
207                  170                 175                 180
208
209  Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
210                  185                 190                 195
211
212  Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
213                  200                 205                 210
214
215  Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
216                  215                 220                 225
217
218  Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro
219                  230                 235                 240
220
221  Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser
222                  245                 250                 255
223
224  Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr
225                  260                 265                 270
226
227  Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg
228                  275                 280                 285
229
230  Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys
231                  290                 295                 300
232
233  Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser
234                  305                 310                 315
235
236  His Lys His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys
237                  320                 325                 330
238
239  Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr
240                  335                 340                 345
241
242  Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln
243                  350                 355                 360
244
245  Arg Gln Val Leu Ser Ile Ser Cys Ile Ile Phe Gly Ile Val Ile
246                  365                 370                 375
247
248  Val Gly Met Phe Cys Ala Ala Phe Tyr Phe Lys Ser Lys Lys Gln
249                  380                 385                 390
250
251  Ala Lys Gln Ile Gln Glu His Leu Lys Glu Ser Gln Asn Gly Lys
252                  395                 400                 405
253
254  Asn Tyr Ser Leu Lys Ala Ser Ser Thr Lys Ser Glu Ser Leu Met
255                  410                 415                 420
256
257  Lys Ser His Val His Leu Gln Asn Tyr Ser Lys Ala Asp Arg His
258                  425                 430                 435
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